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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/062,848

DATE: 02/16/2002

TIME: 13:33:50

Input Set : N:\Crf3\RULE60\10062848.txt

Output Set: N:\CRF3\02152002\J062848.raw

ENTERED

3 <110> APPLICANT: KOSTREWA, Dirk
 4 PASAMONTES, Luis
 5 TOMSCHY, Andrea
 6 van LOON, Adolphus
 7 VOGEL, Kurt
 8 WYSS, Markus
 10 <120> TITLE OF INVENTION: MODIFIED PHYTASES
 12 <130> FILE REFERENCE: Modified Phytases
 14 <140> CURRENT APPLICATION NUMBER: 10/062,848
 C--> 15 <141> CURRENT FILING DATE: 2002-02-01
 17 <150> PRIOR APPLICATION NUMBER: 09/044,718
 18 <151> PRIOR FILING DATE: 1998-03-19
 20 <150> PRIOR APPLICATION NUMBER: EP 97810175.6
 21 <151> PRIOR FILING DATE: 1997-03-25
 23 <160> NUMBER OF SEQ ID NOS: 82
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 444
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Aspergillus niger
 32 <400> SEQUENCE: 1
 33 Ala Ser Arg Asn Gln Ser Ser Cys Asp Thr Val Asp Gln Gly Tyr Gln
 34 1 5 10 15
 36 Cys Phe Ser Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe
 37 20 25 30
 39 Ser Leu Ala Asn Glu Ser Val Ile Ser Pro Glu Val Pro Ala Gly Cys
 40 35 40 45
 42 Arg Val Thr Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro
 43 50 55 60
 45 Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln
 46 65 70 75 80
 48 Gln Asn Ala Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr
 49 85 90 95
 51 Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu
 52 100 105 110
 54 Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr
 55 115 120 125
 57 Arg Asn Ile Val Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile
 58 130 135 140
 60 Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys
 61 145 150 155 160
 63 Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val
 64 165 170 175

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66 Ile Ser Glu Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys
67      180      185      190
69 Thr Val Phe Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe
70      195      200      205
72 Thr Ala Thr Phe Val Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu
73      210      215      220
75 Ser Gly Val Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met
76 225      230      235      240
78 Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser
79      245      250      255
81 Pro Phe Cys Asp Leu Phe Thr His Asp Glu Trp Ile Asn Tyr Asp Tyr
82      260      265      270
84 Leu Gln Ser Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu
85      275      280      285
87 Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu
88      290      295      300
90 Thr His Ser Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp
91 305      310      315      320
93 Ser Ser Pro Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe
94      325      330      335
96 Ser His Asp Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr
97      340      345      350
99 Asn Gly Thr Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln
100     355      360      365
102 Thr Asp Gly Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu
103     370      375      380
105 Tyr Val Glu Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg
106 385      390      395      400
108 Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Val Asp
109     405      410      415
111 Ala Leu Gly Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe
112     420      425      430
114 Ala Arg Ser Gly Gly Asp Trp Ala Glu Cys Phe Ala
115     435      440
118 <210> SEQ ID NO: 2
119 <211> LENGTH: 438
120 <212> TYPE: PRT
121 <213> ORGANISM: Aspergillus terreus
123 <400> SEQUENCE: 2
124 Ser Asp Cys Thr Ser Val Asp Arg Gly Tyr Gln Cys Phe Pro Glu Leu
125 1      5      10      15
127 Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln Asp Glu
128     20      25      30
130 Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr Phe Val
131     35      40      45
133 Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser Lys Thr
134     50      55      60
136 Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala Thr Ala
137 65      70      75      80

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139 Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser Met Gly
140      85      90      95
142 Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp Leu Gly
143      100      105      110
145 Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile Asn Pro
146      115      120      125
148 Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala Glu Lys
149      130      135      140
151 Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His Ala Asn
152 145      150      155      160
154 Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu Gly Thr
155      165      170      175
157 Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe Glu Ala
158      180      185      190
160 Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val Phe Ala
161      195      200      205
163 Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val Gln Leu
164      210      215      220
166 Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe Glu Thr
167 225      230      235      240
169 Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys Asp Leu
170      245      250      255
172 Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser Leu Asp
173      260      265      270
175 Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val Gln Gly
176      275      280      285
178 Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val
179      290      295      300
181 His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro Ala Thr
182 305      310      315      320
184 Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Ser Asn
185      325      330      335
187 Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro
188      340      345      350
190 Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly Tyr Ala
191      355      360      365
193 Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu Met Met
194      370      375      380
196 Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val Asn Asp
197 385      390      395      400
199 Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly Arg Cys
200      405      410      415
202 Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala Gly Gly
203      420      425      430
205 Asn Trp Ala Glu Cys Phe
206      435
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 439
211 <212> TYPE: PRT

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TIME: 13:33:50

Input Set : N:\Crf3\RULE60\10062848.txt

Output Set: N:\CRF3\02152002\J062848.raw

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212 <213> ORGANISM: Aspergillus fumigatus
214 <400> SEQUENCE: 3
215 Ser Lys Ser Cys Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala
216 1 5 10 15
218 Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp
219 20 25 30
221 Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu
222 35 40 45
224 Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys
225 50 55 60
227 Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala Thr
228 65 70 75 80
230 Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu
231 85 90 95
233 Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser
234 100 105 110
236 Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val
237 115 120 125
239 Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu
240 130 135 140
242 Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala
243 145 150 155 160
245 Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu
246 165 170 175
248 Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala
249 180 185 190
251 Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala
252 195 200 205
254 Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr Leu
255 210 215 220
257 Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp Thr
258 225 230 235 240
260 Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu
261 245 250 255
263 Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly
264 260 265 270
266 Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly
267 275 280 285
269 Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val
270 290 295 300
272 Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr
273 305 310 315 320
275 Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser
276 325 330 335
278 Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro
279 340 345 350
281 Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser
282 355 360 365
284 Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met

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Input Set : N:\Crf3\RULE60\10062848.txt

Output Set: N:\CRF3\02152002\J062848.raw

```

285      370      375      380
287 Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp
288 385      390      395      400
290 Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys
291      405      410      415
293 Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly
294      420      425      430
296 Asn Trp Gly Glu Cys Phe Ser
297      435
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 1931
302 <212> TYPE: DNA
303 <213> ORGANISM: Aspergillus nidulans
305 <220> FEATURE:
306 <221> NAME/KEY: CDS
307 <222> LOCATION: (158)..(205)
309 <220> FEATURE:
310 <221> NAME/KEY: CDS
311 <222> LOCATION: (260)..(1600)
313 <400> SEQUENCE: 4
314 tctgtaaccg atagcggacc gactaggcat cggtgatcca caatatctca gacaatgcaa 60
316 ctcagtcgaa tatgaagggc tacagccagc atttaaatac ggccgtctag gtcgggctcc 120
318 ggggatgagg aggagcaggc tcgtgttcat ttcggtc atg gct ttt ttc acg gtc 175
319                               Met Ala Phe Phe Thr Val
320                               1           5
322 gct ctt tcg ctt tat tac ttg cta tcg agg tgagatctct acaatatctg 225
323 Ala Leu Ser Leu Tyr Tyr Leu Leu Ser Arg
324      10      15
326 tctgcttagt tgaattggta cttatctgta caga gtc tct gct cag gcc cca gtc 280
327                               Val Ser Ala Gln Ala Pro Val
328                               20
330 gtc cag aat cat tca tgc aat acg gcg gac ggt gga tat caa tgc ttc 328
331 Val Gln Asn His Ser Cys Asn Thr Ala Asp Gly Gly Tyr Gln Cys Phe
332      25      30      35
334 ccc aat gtc tct cat gtt tgg ggt cag tac tcg ccg tac ttc tcc atc 376
335 Pro Asn Val Ser His Val Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Ile
336 40      45      50      55
338 gag cag gag tca gct atc tct gag gac gtg cct cat ggc tgt gag gtt 424
339 Glu Gln Glu Ser Ala Ile Ser Glu Asp Val Pro His Gly Cys Glu Val
340      60      65      70
342 acc ttt gtg cag gtg ctc tcg cgg cat ggg gct agg tat ccg aca gag 472
343 Thr Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu
344      75      80      85
346 tcg aag agt aag gcg tac tcg ggg ttg att gaa gca atc cag aag aat 520
347 Ser Lys Ser Lys Ala Tyr Ser Gly Leu Ile Glu Ala Ile Gln Lys Asn
348      90      95      100
350 gct acc tct ttt tgg gga cag tat gct ttt ctg gag agt tat aac tat 568
351 Ala Thr Ser Phe Trp Gly Gln Tyr Ala Phe Leu Glu Ser Tyr Asn Tyr
352      105      110      115

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10062848.txt

Output Set: N:\CRF3\02152002\J062848.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:570 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:574 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:578 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:582 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:586 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:590 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:594 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:598 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:602 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:606 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:618 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:622 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:626 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:630 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:634 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:638 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:642 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:646 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
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L:666 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
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L:674 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7